

# Nadim W Alkharouf

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,127  
citations

516710

16  
h-index

526287

27  
g-index

31  
all docs

31  
docs citations

31  
times ranked

1271  
citing authors

#	ARTICLE	IF	CITATIONS
1	Floral Transcriptomes in Woodland Strawberry Uncover Developing Receptacle and Anther Gene Networks. <i>Plant Physiology</i> , 2014, 165, 1062-1075.	4.8	167
2	Laser capture microdissection (LCM) and comparative microarray expression analysis of syncytial cells isolated from incompatible and compatible soybean ( <i>Glycine max</i> ) roots infected by the soybean cyst nematode ( <i>Heterodera glycines</i> ). <i>Planta</i> , 2007, 226, 1389-1409.	3.2	154
3	Laser Capture Microdissection (LCM) and Expression Analyses of <i>Glycine max</i> (Soybean) Syncytium Containing Root Regions Formed by the Plant Pathogen <i>Heterodera glycines</i> (Soybean Cyst Nematode). <i>Plant Molecular Biology</i> , 2005, 59, 965-979.	3.9	114
4	A gene expression analysis of syncytia laser microdissected from the roots of the <i>Glycine max</i> (soybean) genotype PI 548402 (Peking) undergoing a resistant reaction after infection by <i>Heterodera glycines</i> (soybean cyst nematode). <i>Plant Molecular Biology</i> , 2009, 71, 525-567.	3.9	99
5	Syncytium gene expression in <i>Glycine max</i> [PI 88788] roots undergoing a resistant reaction to the parasitic nematode <i>Heterodera glycines</i> . <i>Plant Physiology and Biochemistry</i> , 2010, 48, 176-193.	5.8	74
6	An eFP browser for visualizing strawberry fruit and flower transcriptomes. <i>Horticulture Research</i> , 2017, 4, 17029.	6.3	63
7	Re-annotation of the woodland strawberry ( <i>Fragaria vesca</i> ) genome. <i>BMC Genomics</i> , 2015, 16, 29.	2.8	60
8	Mapping cell fate decisions that occur during soybean defense responses. <i>Plant Molecular Biology</i> , 2011, 77, 513-528.	3.9	59
9	Differences in gene expression amplitude overlie a conserved transcriptomic program occurring between the rapid and potent localized resistant reaction at the syncytium of the <i>Glycine max</i> genotype Peking (PI 548402) as compared to the prolonged and potent resistant reaction of PI 88788. <i>Plant Molecular Biology</i> , 2011, 75, 141-165.	3.9	48
10	LUX ARRHYTHMO mediates crosstalk between the circadian clock and defense in <i>Arabidopsis</i> . <i>Nature Communications</i> , 2019, 10, 2543.	12.8	47
11	Analysis of the genome sequence of <i>Phomopsis longicolla</i> : a fungal pathogen causing <i>Phomopsis</i> seed decay in soybean. <i>BMC Genomics</i> , 2017, 18, 688.	2.8	40
12	Microarray Detection Call Methodology as a Means to Identify and Compare Transcripts Expressed within Syncytial Cells from Soybean ( <i>Glycine max</i> ) Roots Undergoing Resistant and Susceptible Reactions to the Soybean Cyst Nematode ( <i>Heterodera glycines</i> ). <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-30.	3.0	37
13	Transcriptome analysis identifies genes related to the waxy coating on blueberry fruit in two northern-adapted rabbiteye breeding populations. <i>BMC Plant Biology</i> , 2019, 19, 460.	3.6	22
14	Draft genome sequence of <i>Phomopsis longicolla</i> isolate MSPL 10-6. <i>Genomics Data</i> , 2015, 3, 55-56.	1.3	20
15	Generating Genomic Tools for Blueberry Improvement. <i>International Journal of Fruit Science</i> , 2012, 12, 276-287.	2.4	19
16	Proteomic Investigation of <i>Rhizoctonia solani</i> AG 4 Identifies Secretome and Mycelial Proteins with Roles in Plant Cell Wall Degradation and Virulence. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3101-3110.	5.2	18
17	Exocyst components promote an incompatible interaction between <i>Glycine max</i> (soybean) and <i>Heterodera glycines</i> (the soybean cyst nematode). <i>Scientific Reports</i> , 2020, 10, 15003.	3.3	18
18	BBGD: an online database for blueberry genomic data. <i>BMC Plant Biology</i> , 2007, 7, 5.	3.6	17

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19	SoyProLow: A protein database enriched in low abundant soybean proteins. <i>Bioinformatics</i> , 2014, 10, 599-601.	0.5	13
20	Mitogen activated protein kinase (MAPK)-regulated genes with predicted signal peptides function in the Glycine max defense response to the root pathogenic nematode <i>Heterodera glycines</i> . <i>PLoS ONE</i> , 2020, 15, e0241678.	2.5	10
21	MAPKDB: A MAP kinase database for signal transduction element identification. <i>Bioinformatics</i> , 2019, 15, 338-341.	0.5	6
22	The impact of pRAP vectors on plant genetic transformation and pathogenesis studies including an analysis of <i>BRI1-ASSOCIATED RECEPTOR KINASE 1 (BAK1)</i> -mediated resistance. <i>Journal of Plant Interactions</i> , 2021, 16, 270-283.	2.1	5
23	Conserved oligomeric Golgi (COG) complex genes functioning in defense are expressed in root cells undergoing a defense response to a pathogenic infection and exhibit regulation by MAPKs. <i>PLoS ONE</i> , 2021, 16, e0256472.	2.5	5
24	SCNProDB: A database for the identification of soybean cyst nematode proteins. <i>Bioinformatics</i> , 2014, 10, 387-389.	0.5	4
25	Expanding the RNA virome of nematodes and other soil-inhabiting organisms. <i>Virus Evolution</i> , 2022, 8, veac019.	4.9	4
26	Genome-wide functional annotation of <i>Phomopsis longicolla</i> isolate MSPL 10-6. <i>Genomics Data</i> , 2016, 8, 67-69.	1.3	2
27	Compare and Contrast of Differential Gene Expression Software Packages of RNA-Seq. , 2018, , .		1
28	The conserved oligomeric Golgi (COG) complex, a window into plant-pathogen interactions. <i>Journal of Plant Interactions</i> , 2022, 17, 344-360.	2.1	1
29	Data mining of genomic data generated from soybean treated with different phytohormones. , 2016, , .		0
30	A searchable database for the genome of <i>Phomopsis longicolla</i> (isolate MSPL 10-6). <i>Bioinformatics</i> , 2016, 12, 233-236.	0.5	0
31	The heterologous expression of conserved Glycine max (soybean) mitogen activated protein kinase 3 (MAPK3) paralogs suppresses <i>Meloidogyne incognita</i> parasitism in <i>Gossypium hirsutum</i> (upland) Tj ETQq1 1 0.784314 rgBT (Overlock		